

## SEQUENCE LISTING

&lt;110&gt; EXELIXIS, INC.

&lt;120&gt; CCT6s AS MODIFIERS OF THE RB PATHWAY AND METHODS OF USE

&lt;130&gt; EX03-086C-PC

&lt;150&gt; US 60/428,872

&lt;151&gt; 2002-11-25

&lt;160&gt; 9

&lt;170&gt; PatentIn version 3.2

&lt;210&gt; 1

&lt;211&gt; 2562

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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 35 40 45

Ser Gly Ala Gly Asp Ile Lys Leu Thr Lys Asp Gly Asn Val Leu Leu  
 50 55 60

His Glu Met Gln Ile Gln His Pro Thr Ala Ser Leu Ile Ala Lys Val  
 65 70 75 80

Ala Thr Ala Gln Asp Asp Ile Thr Gly Asp Gly Thr Thr Ser Asn Val  
 85 90 95

Leu Ile Ile Gly Glu Leu Leu Lys Gln Ala Asp Leu Tyr Ile Ser Glu  
 100 105 110

Gly Leu His Pro Arg Ile Ile Thr Glu Gly Phe Glu Ala Ala Lys Glu  
 115 120 125

Lys Ala Leu Gln Phe Leu Glu Glu Val Lys Val Ser Arg Glu Met Asp  
 130 135 140

Arg Glu Thr Leu Ile Asp Val Ala Arg Thr Ser Leu Arg Thr Lys Val  
 145 150 155 160

His Ala Glu Leu Ala Asp Val Leu Thr Glu Ala Val Val Asp Ser Ile  
 165 170 175

Leu Ala Ile Lys Lys Gln Asp Glu Pro Ile Asp Leu Phe Met Ile Glu  
 180 185 190

Ile Met Glu Met Lys His Lys Ser Glu Thr Asp Thr Ser Leu Ile Arg

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Lys Thr Glu Val Asn Ser Gly Phe Phe Tyr Lys Ser Ala Glu Glu Arg		
245	250	255
Glu Lys Leu Val Lys Ala Glu Arg Lys Phe Ile Glu Asp Arg Val Lys		
260	265	270
Lys Ile Ile Glu Leu Lys Arg Lys Val Cys Gly Asp Ser Asp Lys Gly		
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Phe Val Val Ile Asn Gln Lys Gly Ile Asp Pro Phe Ser Leu Asp Ala		
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Leu Ser Lys Glu Gly Ile Val Ala Leu Arg Arg Ala Lys Arg Arg Asn		
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Met Glu Arg Leu Thr Leu Ala Cys Gly Gly Val Ala Leu Asn Ser Phe		
325	330	335
Asp Asp Leu Ser Pro Asp Cys Leu Gly His Ala Gly Leu Val Tyr Glu		
340	345	350
Tyr Thr Leu Gly Glu Glu Lys Phe Thr Phe Ile Glu Lys Cys Asn Asn		
355	360	365
Pro Arg Ser Val Thr Leu Leu Ile Lys Gly Pro Asn Lys His Thr Leu		
370	375	380
Thr Gln Ile Lys Asp Ala Val Arg Asp Gly Leu Arg Ala Val Lys Asn		
385	390	395
Ala Ile Asp Asp Gly Cys Val Val Pro Gly Ala Gly Ala Val Glu Val		
405	410	415
Ala Met Ala Glu Ala Leu Ile Lys His Lys Pro Ser Val Lys Gly Arg		
420	425	430
Ala Gln Leu Gly Val Gln Ala Phe Ala Asp Ala Leu Leu Ile Ile Pro		
435	440	445

Lys Val Leu Ala Gln Asn Ser Gly Phe Asp Leu Gln Glu Thr Leu Val  
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Lys Ile Gln Ala Glu His Ser Glu Ser Gly Gln Leu Val Gly Val Asp  
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Leu Asn Thr Gly Glu Pro Met Val Ala Ala Glu Val Gly Val Trp Asp  
 485 490 495

Asn Tyr Cys Val Lys Lys Gln Leu Leu His Ser Cys Thr Val Ile Ala  
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Thr Asn Ile Leu Leu Val Asp Glu Ile Met Arg Ala Gly Met Ser Ser  
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Leu Lys Gly  
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Gly Ala Gly Asp Ile Lys Leu Thr Lys Asp Gly Asn Val Leu Leu Asp  
 50 55 60

Glu Met Gln Ile Gln His Pro Thr Ala Ser Leu Ile Ala Lys Val Ala  
 65 70 75 80

Thr Ala Gln Asp Gly Val Thr Gly Asp Gly Thr Thr Thr Asn Val Leu  
 85 90 95

Ile Ile Gly Glu Leu Leu Lys Gln Ala Asp Leu Tyr Ile Ser Glu Gly  
 100 105 110

Leu His Pro Arg Ile Ile Ala Glu Gly Phe Glu Ala Ala Lys Ile Lys  
 115 120 125

Ala Leu Glu Val Leu Glu Glu Val Lys Val Thr Lys Glu Met Lys Arg  
 130 135 140

Lys Ile Leu Leu Asp Val Ala Arg Thr Ser Leu Gln Thr Lys Val His  
 145 150 155 160

Ala Glu Leu Ala Asp Val Leu Thr Glu Val Val Val Asp Ser Leu Phe  
 165 170 175

Pro Val Arg Arg Pro Pro Tyr Pro Ile Asp Leu Phe Met Val Glu Ile  
 180 185 190

Met Glu Met Lys His Lys Leu Gly Thr Asp Thr Lys Leu Ile Gln Gly  
 195 200 205

Leu Val Leu Asp His Gly Ala Arg His Pro Asp Met Lys Lys Arg Val  
 210 215 220

Glu Asp Ala Phe Ile Leu Ile Cys Asn Val Ser Leu Glu Tyr Glu Lys  
 225 230 235 240

Thr Glu Val Asn Ser Ala Phe Phe Tyr Lys Thr Ala Glu Glu Lys Glu  
 245 250 255

Lys Leu Val Lys Ala Glu Arg Lys Phe Ile Glu Asp Arg Val Gln Lys  
 260 265 270

Ile Ile Asp Leu Lys Asp Lys Val Cys Ala Gln Ser Asn Lys Gly Phe  
 275 280 285

Val Val Ile Asn Gln Lys Gly Ile Asp Pro Phe Ser Leu Asp Ser Leu  
 290 295 300

Ala Lys His Gly Ile Val Ala Leu Arg Arg Ala Lys Arg Arg Asn Met  
 305 310 315 320

Glu Arg Leu Ser Leu Ala Cys Gly Gly Met Ala Val Asn Ser Phe Glu  
 325 330 335

Asp Leu Thr Val Asp Cys Leu Gly His Ala Gly Leu Val Tyr Glu Tyr  
 340 345 350

Thr Leu Gly Glu Glu Lys Phe Thr Phe Ile Glu Glu Cys Val Asn Pro  
 355 360 365

Cys Ser Val Thr Leu Leu Val Lys Gly Pro Asn Lys His Thr Leu Thr  
 370 375 380

Gln Val Lys Asp Ala Ile Arg Asp Gly Leu Arg Ala Ile Lys Asn Ala  
 385 390 395 400

Ile Glu Asp Gly Cys Met Val Pro Gly Ala Gly Ala Ile Glu Val Ala  
 405 410 415

Met Ala Glu Ala Leu Val Thr Tyr Lys Asn Ser Ile Lys Gly Arg Ala  
 420 425 430

Arg Leu Gly Val Gln Ala Phe Ala Asp Ala Leu Leu Ile Ile Pro Lys  
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Val Leu Ala Gln Asn Ala Gly Tyr Asp Pro Gln Glu Thr Leu Val Lys  
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Val Gln Ala Glu His Val Glu Ser Lys Gln Leu Val Gly Val Asp Leu  
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Asn Thr Gly Glu Pro Met Val Ala Ala Asp Ala Gly Val Trp Asp Asn  
 485 490 495

Tyr Cys Val Lys Lys Gln Leu Leu His Ser Cys Thr Val Ile Ala Thr  
 500 505 510

Asn Ile Leu Leu Val Asp Glu Ile Met Arg Ala Gly Met Ser Ser Gln  
 515 520 525

Met Met Ile Glu Phe Lys Ile Asn Pro Ser Arg Arg  
 530 535 540

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